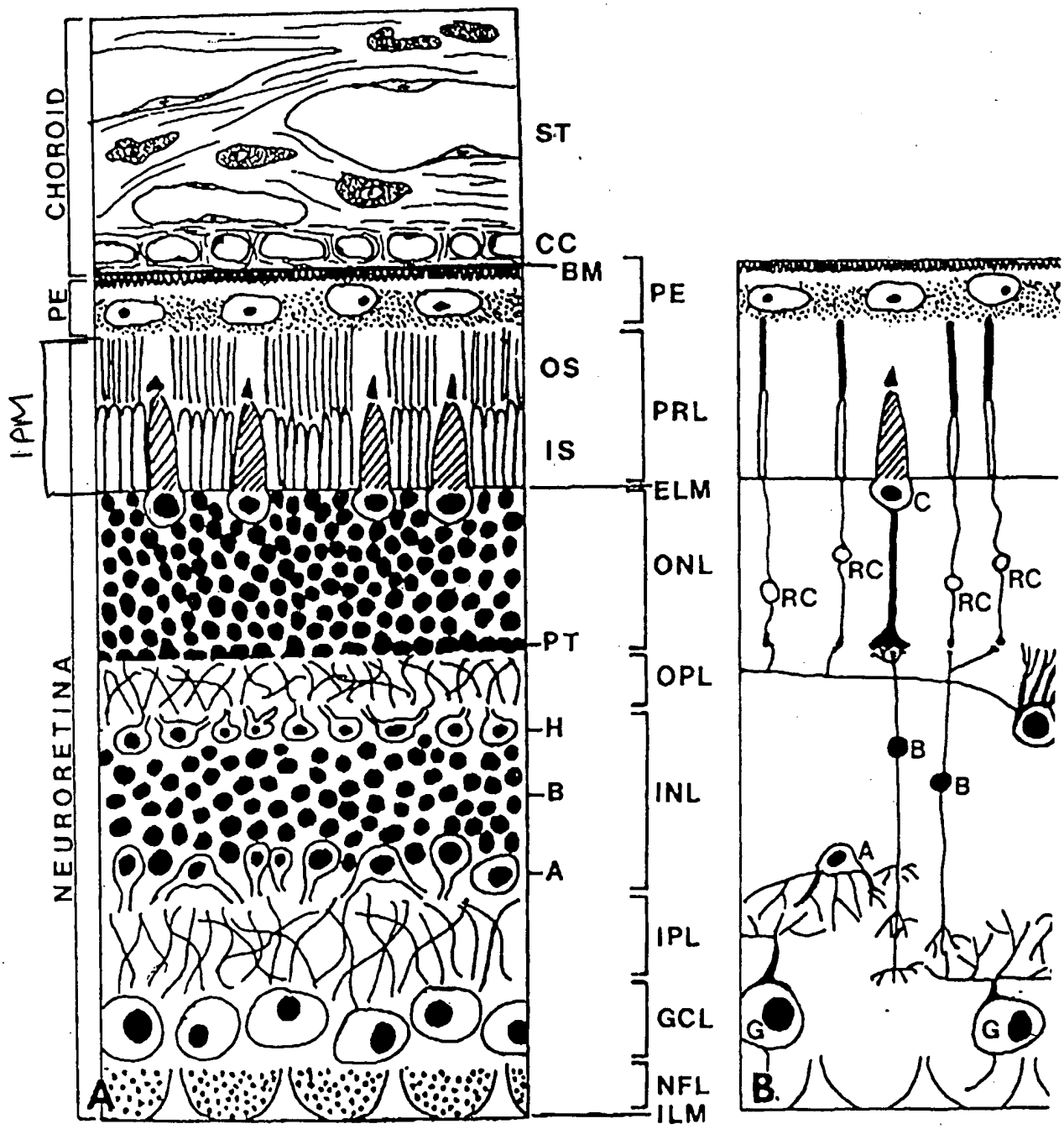

Fig. 1

Monkey IPM 150

```
001  ATTTTCTTTCCGAACGGGGTTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGCCAGTCTTCAAGCTTATTATAGATTGAGAGTGTGTCAGGAAG
       I  F  F  P  N  G  V  K  V  C  P  Q  E  S  M  K  Q  I  L  A  S  L  Q  A  Y  Y  R  L  R  V  C  Q  E

101  CAGTATGGGAAGCATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGACTGGGTCAGCTTCTGCCAGCAGGAGACCTTCTGCCTCTT
       A  V  W  E  A  Y  R  I  F  L  D  R  I  P  D  T  G  E  Y  Q  D  W  V  S  F  C  Q  Q  E  T  F  C  L  F

201  TGACATCGGACAAAACTTCAGCAATTCCCAGGAGCACCTGGATCTTCTCCAGCAGAGAATAAAACAGAGAAGTTTCCCTGAGAGAAAAGATGAAGTATCT
       D  I  G  Q  N  F  S  N  S  Q  E  H  L  D  L  L  Q  Q  R  I  K  Q  R  S  F  P  E  R  K  D  E  V  S

301  ACAGAGAAGACATTGGGAGAGCCTAGTGAAACCATTGTGGTTTCAACAGATGTTGCCAGCGTCTCACTTGGGCCTTTCCCTGTCACTCCTGATGACACCC
       T  E  K  T  L  G  E  P  S  E  T  I  V  V  S  T  D  V  A  S  V  S  L  G  P  F  P  V  T  P  D  D  T

401  TCCTCAATGAAATTCTCGATAATGCACTCAACGACACCAAGATGCCTACAACAGAAAGAGAAACAGAACTCGCTGTGTCTGAGGAGCAGAGGGTGGAGCT
       L  L  N  E  I  L  D  N  A  L  N  D  T  K  M  P  T  T  E  R  E  T  E  L  A  V  S  E  E  Q  R  V  E  L

501  CAGCATCTCTCTGATAAACCAGAGGTTCAAGGCAGAGCTCGCTGACTCTCAGTCA
       S  I  S  L  I  N  Q  R  F  K  A  E  L  A  D  S  Q  S
```

Fig. 2

Human IPM 150

001 TAAACCAAGAAGGTTATCCTCAATCATCTGGTATCAATATATAATTATTTTTCCTTTNTGTTACTTTTTAATGAGATTTGAGGTTGTTCTGTGATTGTTA

101 TCAGAATTACCATGCACAAAAGCCAGAATGTATTTGGAAACTAGAAGAGCTATTTTTGTTTTTGGATTTTTCTCCAAGTTCAAGGAACTAAAGATATCT

M Y L E T R R A I F V F W I F L Q V Q G T K D I

201 CCATTAACATATACCATTCTGAAACTAAAGACATAGACAATCCCCCAAGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTATGAG

S I N I Y H S E T K D I D N P P R N E T T E S T E K M Y K M S T M R

301 ACGAATATTCGATTTGGCAAAGCATCGAACAAAAAGATCCGCATTTTTCCCAACGGGGGTTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGAC

R I F D L A K H R T K R S A F F P T G V K V C P Q E S M K Q I L D

401 AGTCTTCAAGCTTATTATAGATTGAGAGTGTGTCAGGAAGCAGTATGGAAGCATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGG

S L Q A Y Y R L R V C Q E A V W E A Y R I F L D R I P D T G E Y Q

501 ACTGGGTCAGCATCTGCCAGCAGGAGACCTTCTGCCTCTTTGACATTGGAAAAAACTTCAGCAATTCCCAGGAGCACCTGGATCTTCTCCAGCAGAGAAT

D W V S I C Q Q E T F C L F D I G K N F S N S Q E H L D L L Q Q R I

601 AAAACAGAGAAGTTTCCCTGACAGAAAAGATGAAATATCTGCAGAGAAGACATTGGGAGAGCCTGGTGAAACCATTGTCATTTCAACAGATGTTGCCAAC

K Q R S F P D R K D E I S A E K T L G E P G E T I V I S T D V A N

701 GTCTCACTTGGGCCTTTCCCTCTCACTCCTGATGACACCCTCCTCAATGAAATTCTCGATAATACACTCAACGACACCAAGATGCCTACAACAGAAAGAG

V S L G P F P L T P D D T L L N E I L D N T L N D T K M P T T E R

801 AAACAGAATTCGCTGTGTTGGAGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGGTAAACCAGAAGTTCAAGGCAGAGCTCGCTGACTCCCAGTCCCCATA

E T E F A V L E E Q R V E L S V S L V N Q K F K A E L A D S Q S P Y

901 TTACCAGGAGCTAGCAGGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAACTTCCAGGATTCAAAAAAATCCATGTGTTAGGATTTAGACCAAAG

Y Q E L A G K S Q L Q M Q K I F K K L P G F K K I H V L G F R P K

1001 AAAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAGCAAAAAGCCCTGCAAGTGACCTCCTGTCTT

K E K D G S S S T E M Q L T A I F K R H S A E A K S P A S D L L S

1101 TTGATTCCAACAAAATTGAAAGTGAGGAAGTCTATCATGGAACCATGGAGGAGGACAAGCAACCAGAAATCTATCTCACAGCTACAGACCTCAAAAGGCT

F D S N K I E S E E V Y H G T M E E D K Q P E I Y L T A T D L K R L

1201 GATCAGCAAAGCACTAGAGGAAGAACAATCTTTGGATGTGGGGACAATTCAGTTCACTGATGAAATTGCTGGATCACTGCCAGCCTTTGGTCCTGACACC

I S K A L E E E Q S L D V G T I Q F T D E I A G S L P A F G P D T

1301 CAATCAGAGCTGCCCACATCTTTTGCTGTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCCTCCTGTTGAACCCCAGCTTGAGACAGTGGACGGAG

Q S E L P T S F A V I T E D A T L S P E L P P V E P Q L E T V D G

1401 CAGAGCATGGTCTACCTGACACTTCTTGGTCTCCACCTGCTATGGCCTCTACCTCCCTGTCAGAAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTC

A E H G L P D T S W S P P A M A S T S L S E A P P F F M A S S I F S

1501 TCTGACTGATCAAGGCACCACAGATACAATGGCCACTGACCAGACAATGCTAGTACCAGGGCTCACCATCCCCACCAGTGATTATTCTGCAATCAGCCAA

L T D Q G T T D T M A T D Q T M L V P G L T I P T S D Y S A I S Q

1601 CTGGCTCTGGGAATTTCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTCAGACACCTAGATGAAATGGATCTGT

L A L G I S H P P A S S D D S R S S A G G E D M V R H L D E M D L

1701 CTGACACTCCTGCCCCATCTGAGGTACCAGAGCTCAGCGAATATGTTTCTGTCCCAGATCATTTCTTGGAGGATACCACTCCTGTCTCAGCTTTACAGTA

S D T P A P S E V P E L S E Y V S V P D H F L E D T T P V S A L Q Y

1801 TATCACCACTAGTTCTATGACCATTGCCCCCAAGGGCCGAGAGCTGGTAGTGTTCTTCAGTCTGCGTGTTGCTAACATGGCCTTCTCCAACGACCTGTTC

I T T S S M T I A P K G R E L V V F F S L R V A N M A F S N D L F

1901 AACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGCTGGTTCCATATCTACGATCCAATCTTACAGGATTTAAGCAACTTGAAA

N K S S L E Y R A L E Q Q F T Q L L V P Y L R S N L T G F K Q L E

2001 TACTTAACTTCAGAAACGGGAGTGTGATTGTGAATAGCAAAATGAAGTTTGCTAAGTCTGTGCCGTATAACCTCACCAAGGCTGTGCACGGGGTCTTGGA

I L N F R N G S V I V N S K M K F A K S V P Y N L T K A V H G V L E

2101 GGATTTTCGTTCTGCTGCAGCCCAACAACTCCATCTGGAAATAGACAGCTACTCTCTCAACATTGAACCAGCTGATCAAGCAGATCCCTGCAAGTTCCTG

D F R S A A A Q Q L H L E I D S Y S L N I E P A D Q A D P C K F L

2201 GCCTGCGGCGAATTTGCCCAATGTGTAAAGAACGAACGGACTGAGGAAGCGGAGTGTCGCTGCAAACCAGGATATGACAGCCAGGGGAGCCTGGACGGTC

A C G E F A Q C V K N E R T E E A E C R C K P G Y D S Q G S L D G

2301 TGGAACCAGGCCTCTGTGGCCTGGCACAAAGGAATGCGAGGTCCTCCAGGGAAAGGGAGCTCCATGCGGTTCCAGATCACTCTGAAAATCAAGCATACAA

L E P G L C G L A Q R N A R S S R E R E L H A V P D H S E N Q A Y K

2401 AACTAGTGTTAAAAGTTCCAAAATCAACAAAATAACAAGGTAATCAGTAAAAGAAATTCTGAATTACTGACCGTAGAATATGAAGAATTTAACCATCAAG

T S V K S S K I N K I T R STOP

2501 ATTGGGAAGGAAATTAAAAACTGAAAATGTACAATTATCACTTAGGCTATCTCAAGAGAGATGATTTGCCTTCTCAAGGAAAATGGAGACAGGCATATTC

2601 ATGGGTCATCAAAATCCAGACATACAGTCAACACTGAGAATCAGCACACACCATATTTCAAATATAGAAGAGTCATGTACTTGGCAACCAGTAAATTCTG

2701 AAAAAAAAGACACTTACTTATTATTAAAACCCCAAATGCAATCAGCGAAACATATTTTTACTATTCTTGGATGATAGTCAAAATGATCATAAGCCAGGTT

2801 TGCTTCCACCTTCCCTGAAAATTTTACTCACAGATCATTTGCAACAAGCATAGCTTACTTATTGTTTAGGGACTGAACAATTTATTGGGAAGCAAACTCT

2901 TTATATGCTAGAAAGTACATTTAAAAGATGACTACTTACGCAGGGAGATGCAGGTCTCTCTAAACGCATGAATGTATGTAGTGTGTAGGCACTGTAGTGA

3001 GTGTATATATGCTCCACACTACGTCTGATAAACACAAACCTCAGTATTCAGTTATTAGGCACACTAGTTTTATACGCAACTACTGCTTACATAGTAGACT

3101 GTTTTGTTGCCAATAATCTTTGAATTGTTCTTTAAAAGAAACTGAGGTTCAGATACACATACCATGGAAAAATCTTACTTTTCTTGTTACTACACAAAGC

3201 TATTTTAAAGAAGATGCTATGTTGGGAGAAGGGCGAAGTTGTACTATATGACATAATCAAT

Fig. 3

Human IPM 200

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001  CGGGYWAYTTTGAAAGGACAACCATTTTTCTTTCCGCTAATTTATAATGGTTTTGAAGTGGTTGTTCATTCTCAAACATAGACTTTTAAATGTTAGGTCT
101  TTCCTATAACTCTTTGTTATTGGAAGTTTCAAGGATTTGGACACTCAATTAAGGATTCTGTCCTCTCCTCATTCCTTTGGTTTTGGCCCAAATGATTATG
                                                                                                 M  I  M

201  TTTCCTCTTTTTGGGAAGATTTCTCTGGGTATTTTGATATTTGTCCTGATAGAAGGAGACTTTCCATCATTAACAGCACAAACCTACTTATCTATAGAGG
      F  P  L  F  G  K  I  S  L  G  I  L  I  F  V  L  I  E  G  D  F  P  S  L  T  A  Q  T  Y  L  S  I  E

301  AGATCCAAGAACCCAAGAGTGCAGTTTCTTTTCTCCTGCCTGAAGAATCAACAGACCTTTCTCTAGCTACCAAAAAGAAACAGCCTCTGGACCGCAGAGA
     E  I  Q  E  P  K  S  A  V  S  F  L  L  P  E  E  S  T  D  L  S  L  A  T  K  K  K  Q  P  L  D  R  R  E

401  AACTGAAAGACAGTGGTTAATCAGAAGGCGGAGATCTATTCTGTTTCCTAATGGAGTGAAAATCTGCCCAGATGAAAGTGTTGCAGAGGCTGTGGCAAAT
       T  E  R  Q  W  L  I  R  R  R  R  S  I  L  F  P  N  G  V  K  I  C  P  D  E  S  V  A  E  A  V  A  N

501  CATGTGAAGTATTTTAAAGTCCGAGTGTGTCAGGAAGCTGTCTGGGAAGCCTTCAGGACTTTTTGGGATCGACTTCCTGGGCGTGAGGAATATCATTACT
      H  V  K  Y  F  K  V  R  V  C  Q  E  A  V  W  E  A  F  R  T  F  W  D  R  L  P  G  R  E  E  Y  H  Y

601  GGATGAATTTGTGTGAGGATGGAGTCACAAGTATATTTGAAATGGGCACAAATTTTAGTGAATCTGTGGAACATAGAAGCTTAATCATGAAGAAACTGAC
     W  M  N  L  C  E  D  G  V  T  S  I  F  E  M  G  T  N  F  S  E  S  V  E  H  R  S  L  I  M  K  K  L  T

701  TTATGCAAAGGAAACTGTAAGCAGCTCTGAACTGTCTTCTCCAGTTCCTGTTGGTGATACTTCAACATTGGGAGACACTACTCTCAGTGTTCCACATCCA
       Y  A  K  E  T  V  S  S  S  E  L  S  S  P  V  P  V  G  D  T  S  T  L  G  D  T  T  L  S  V  P  H  P

801  GAGGTGGACGCCTATGAAGGTGCCTCAGAGAGCAGCTTGGAAAGGCCAGAGGAGAGTATTAGCAATGAAATTGAGAATGTGATAGAAGAAGCCACAAAAC
      E  V  D  A  Y  E  G  A  S  E  S  S  L  E  R  P  E  E  S  I  S  N  E  I  E  N  V  I  E  E  A  T  K

901  CAGCAGGTGAACAGATTGCAGAATTCAGTATCCACCTTTTGGGGAAGCAGTACAGGGAAGAACTACAGGATTCCTCCAGCTTTCACCACCAGCACCTTGA
     P  A  G  E  Q  I  A  E  F  S  I  H  L  L  G  K  Q  Y  R  E  E  L  Q  D  S  S  S  F  H  H  Q  H  L  E

1001 AGAAGAATTTATTTCAGAGGTTGAAAATGCATTTACTGGGTTACCAGGCTACAAGGAAATTCGTGTACTTGAATTTAGGTCCCCCAAGGAAAATGACAGT
       E  E  F  I  S  E  V  E  N  A  F  T  G  L  P  G  Y  K  E  I  R  V  L  E  F  R  S  P  K  E  N  D  S

1101 GGCGTAGATGTTTACTATGCAGTTACCTTCAATGGTGAGGCCATCAGCAATACCACCTGGGACCTCATTAGCCTTCACTCCAACAAGGTGGAAAACCATG
      G  V  D  V  Y  Y  A  V  T  F  N  G  E  A  I  S  N  T  T  W  D  L  I  S  L  H  S  N  K  V  E  N  H

1201 GCCTTGTGGAACTGGATGATAAACCCACTGTTGTTTATACAATCAGTAACTTCAGAGATTATATTGCTGAGACATTGCAGCAGAATTTTTTGCTGGGGAA
     G  L  V  E  L  D  D  K  P  T  V  V  Y  T  I  S  N  F  R  D  Y  I  A  E  T  L  Q  Q  N  F  L  L  G  N

1301 CTCTTCCTTGAATCCAGATCCTGATTCCCTGCAGCTTATCAATGTGAGAGGAGTTTTGCGTCACCAAACTGAAGATCTAGTTTGGAACACCCAAAGTTCA
       S  S  L  N  P  D  P  D  S  L  Q  L  I  N  V  R  G  V  L  R  H  Q  T  E  D  L  V  W  N  T  Q  S  S

1401 AGTCTTCAGGCAACGCCGTCATCTATTCTGGATAATACCTTTCAAGCTGCATGGCCCTCAGCAGATGAATCCATCACCAGCAGTATTCCACCACTTGATT
      S  L  Q  A  T  P  S  S  I  L  D  N  T  F  Q  A  A  W  P  S  A  D  E  S  I  T  S  S  I  P  P  L  D

1501 TCAGCTCTGGTCCTCCCTCAGCCACTGGCAGGGAACTCTGGTCAGAAAGTCCTTTGGGTGATTTAGTGTCTACACACAAATTAGCCTTTCCCTCGAAGAT
     F  S  S  G  P  P  S  A  T  G  R  E  L  W  S  E  S  P  L  G  D  L  V  S  T  H  K  L  A  F  P  S  K  M

1601 GGGCCTCAGCTCTTCCCCAGAGGTTTTAGAGGTTAGCAGCTTGACTCTTCATTCTGTCACCCCGGCAGTGCTTCAGACTGGCTTGCCTGTGGCTTCTGAG
       G  L  S  S  S  P  E  V  L  E  V  S  S  L  T  L  H  S  V  T  P  A  V  L  Q  T  G  L  P  V  A  S  E

1701 GAAAGGACTTCTGGATCTCACTTGGTAGAAGATGGATTAGCCAATGTTGAAGAGTCAGAAGATTTTCTTTCTATTGATTCATTGCCTTCAAGTTCATTCA
      E  R  T  S  G  S  H  L  V  E  D  G  L  A  N  V  E  E  S  E  D  F  L  S  I  D  S  L  P  S  S  S  F

1801 CTCAACCTGTGCCAAAAGAAACAATACCATCCATGGAAGACTCTGATGTGTCCTTAACATCTTCACCATATCTGACCTCTTCTATACCTTTTGGCTTGGA
     T  Q  P  V  P  K  E  T  I  P  S  M  E  D  S  D  V  S  L  T  S  S  P  Y  L  T  S  S  I  P  F  G  L  D

1901 CTCCTTGACCTCCAAAGTCAAAGACCAATTAAAAGTGAGCCCTTTCCTGCCAGATGCATCCATGGAAAAAGAGTTAATATTTGACGGTGGTTTAGGTTCA
       S  L  T  S  K  V  K  D  Q  L  K  V  S  P  F  L  P  D  A  S  M  E  K  E  L  I  F  D  G  G  L  G  S

2001 GGGTCTGGGCAAAAGGTAGATCTGATTACTTGGCCATGGAGTGAGACTTCATCAGAGAAGAGCGCCGAACCACTGTCCAAGCCGTGGCTTGAAGATGATG
      G  S  G  Q  K  V  D  L  I  T  W  P  W  S  E  T  S  S  E  K  S  A  E  P  L  S  K  P  W  L  E  D  D

2101 ATTCACTTTTGCCAGCTGAGATTGAAGACAAGAAACTAGTTTTAGTTGACAAAATGGATTCCACAGACCAAATTAGTAAGCACTCAAAATATGAACATGA
     D  S  L  L  P  A  E  I  E  D  K  K  L  V  L  V  D  K  M  D  S  T  D  Q  I  S  K  H  S  K  Y  E  H  D

2201 TGACAGATCCACACACTTTCCAGAGGAAGAGCCTCTTAGTGGGCCTGCTGTGCCCATCTTCGCAGATACTGCAGCTGAATCTGCGTCTCTAACCCTCCCC
       D  R  S  T  H  F  P  E  E  E  P  L  S  G  P  A  V  P  I  F  A  D  T  A  A  E  S  A  S  L  T  L  P

2301 AAGCACATATCAGAAGTACCTGGTGTTGATGATTGCTCAGTTACCAAAGCACCTCTTATACTGACATCTGTAGCAATCTCTGCCTCTACTGATAAATCAG
      K  H  I  S  E  V  P  G  V  D  D  C  S  V  T  K  A  P  L  I  L  T  S  V  A  I  S  A  S  T  D  K  S

2401 ATCAGGCAGATGCCATCCTAAGGGAGGATATGGAACAAATTACTGAGTCATCCAACTATGAATGGTTTGACAGTGAGGTTTCAATGGTAAAGCCAGATAT
     D  Q  A  D  A  I  L  R  E  D  M  E  Q  I  T  E  S  S  N  Y  E  W  F  D  S  E  V  S  M  V  K  P  D  M

2501 GCAAACTTTGTGGACTATATTGCCAGAATCAGAGAGAGTTTGGACAAGAACTTCTTCCCTAGAGAAATTGTCCAGAGACATATTGGCAAGTACACCACAG
       Q  T  L  W  T  I  L  P  E  S  E  R  V  W  T  R  T  S  S  L  E  K  L  S  R  D  I  L  A  S  T  P  Q

2601 AGTGCTGACAGGCTCTGGTTATCTGTGACACAGTCTACCAAATTGCCTCCAACCACAATCTCCACCCTGCTAGAGGATGAAGTAATTATGGGTGTACAGG
      S  A  D  R  L  W  L  S  V  T  Q  S  T  K  L  P  P  T  T  I  S  T  L  L  E  D  E  V  I  M  G  V  Q

2701 ATATTTCGTTAGAACTGGACCGGATAGGCACAGATTACTATCAGCCTGAGCAAGTCCAAGAGCAAAATGGCAAGGTTGGTAGTTATGTGGAAATGTCAAC
     D  I  S  L  E  L  D  R  I  G  T  D  Y  Y  Q  P  E  Q  V  Q  E  Q  N  G  K  V  G  S  Y  V  E  M  S  T

2801 AAGTGTTCACTCCACAGAGATGGTTAGTGTGGCTTGGCCCACAGAAGGAGGAGATGACTTGAGTTATACCCAGACTTCAGGAGCTTTGGTGGTTTTCTTC
       S  V  H  S  T  E  M  V  S  V  A  W  P  T  E  G  G  D  D  L  S  Y  T  Q  T  S  G  A  L  V  V  F  F

2901 AGCCTCCGAGTGACTAACATGATGTTTTCAGAAGATCTGTTTAATAAAAACTCCTTGGAGTATAAAGCCCTGGAGCAAAGATTCTTAGAATTGCTGGTTC
      S  L  R  V  T  N  M  M  F  S  E  D  L  F  N  K  N  S  L  E  Y  K  A  L  E  Q  R  F  L  E  L  L  V
```

Fig 4A

```
3001  CCTATCTCCAGTCAAATCTCACGGGGTTCCAGAACTTAGAAATCCTCAACTTCAGAAATGGCAGCATTGTGGTGAACAGTCGAATGAAGTTTGCCAATTC
      P  Y  L  Q  S  N  L  T  G  F  Q  N  L  E  I  L  N  F  R  N  G  S  I  V  V  N  S  R  M  K  F  A  N  S

3101  TGTCCCTCCTAACGTCAACAATGCGGTGTACATGATTCTGGAAGACTTTTGTACCACTGCCTACAATACCATGAACTTGGCTATTGATAAATACTCTCTT
       V  P  P  N  V  N  N  A  V  Y  M  I  L  E  D  F  C  T  T  A  Y  N  T  M  N  L  A  I  D  K  Y  S  L

3201  GATGTGGAATCAGGTGATGAAGCCAACCCTTGCAAGTTTCAGGCCTGTAATGAATTTTCAGAGTGTCTGGTCAACCCCTGGAGTGGAGAAGCAAAGTGCA
       D  V  E  S  G  D  E  A  N  P  C  K  F  Q  A  C  N  E  F  S  E  C  L  V  N  P  W  S  G  E  A  K  C

3301  GATGCTTCCCTGGATACCTGAGTGTGGAAGAACGGCCCTGTCAGAGTCTCTGTGACCTACAGCCTGACTTCTGCTTGAATGATGGAAAGTGTGACATTAT
      R  C  F  P  G  Y  L  S  V  E  E  R  P  C  Q  S  L  C  D  L  Q  P  D  F  C  L  N  D  G  K  C  D  I  M

3401  GCCTGGGCACGGGGCCATTTGTAGGTGCCGGGTGGGTGAGAACTGGTGGTACCGAGGCAAGCACTGTGAGGAATTTGTGTCTGAGCCCGTGATCATAGGC
        P  G  H  G  A  I  C  R  C  R  V  G  E  N  W  W  Y  R  G  K  H  C  E  E  F  V  S  E  P  V  I  I  G

3501  ATCACTATTGCCTCCGTGGTTGGACTTCTTGTCATCTTTTCTGCTATCATCTACTTCTTCATCAGGACTCTTCAAGCACACCATGACAGGAGTGAAAGAG
       I  T  I  A  S  V  V  G  L  L  V  I  F  S  A  I  I  Y  F  F  I  R  T  L  Q  A  H  H  D  R  S  E  R

3601  AGAGTCCCTTCAGTGGCTCCAGCAGGCAGCCTGACAGCCTCTCATCTATTGAGAATGCTGTGAAGTACAACCCCGTGTATGAAAGTCACAGGGCTGGATG
      E  S  P  F  S  G  S  S  R  Q  P  D  S  L  S  S  I  E  N  A  V  K  Y  N  P  V  Y  E  S  H  R  A  G  C

3701  TGAGAAGTATGAGGGACCCTATCCTCAGCATCCCTTCTACAGCTCTGCTAGCGGAGACGTGATTGGTGGGCTGAGCAGAGAAGAAATCAGACAGATGTAT
        E  K  Y  E  G  P  Y  P  Q  H  P  F  Y  S  S  A  S  G  D  V  I  G  G  L  S  R  E  E  I  R  Q  M  Y

3801  GAGAGCAGTGAGCTTTCCAGAGAGGAAATTCAAGAGAGAATGAGAGTTTTGGAACTGTATGCCAATGATCCTGAGTTTGCAGCTTTTGTGAGAGAGCAAC
       E  S  S  E  L  S  R  E  E  I  Q  E  R  M  R  V  L  E  L  Y  A  N  D  P  E  F  A  A  F  V  R  E  Q

3901  AAGTGGAAGAGGTTTAACCAAAACTCCTGTTCTGAAACTGATTAGAAGCCTGGAGAAGATGGAGATTACTTGTTACTTATGTCATATAATTAACCTGGAT
      Q  V  E  E  V  STOP

4001  TTTAAACACTGTTGGAAGAAGAGNTTTCTATGAAAAAATTAAATATAGGGCACACTGTTTTTTTTTCAGCTTAAGNTTTCAGAATGTAGTNAGAGATGTW
4101  MCATTTTTATTTCTATAAAGACTGAATGCTGTGTTTAAATAATTGAAAACTACGTTAAAAAAAAA
```

Fig. 4B

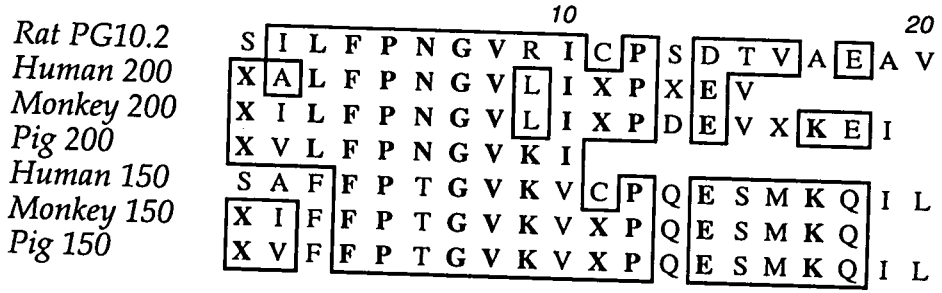

Fig. 5